

Figure 2A

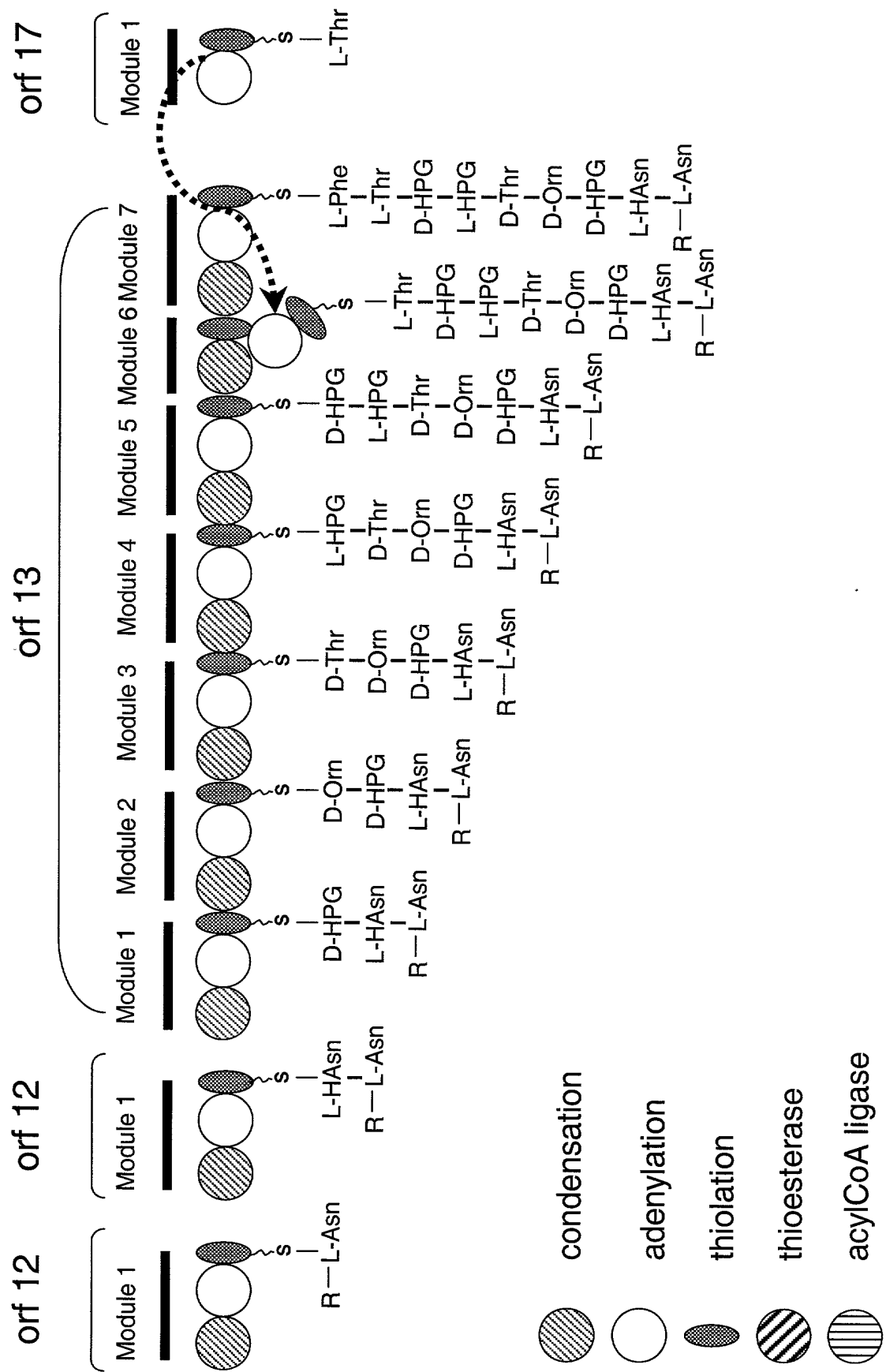


Figure 2A cont'd

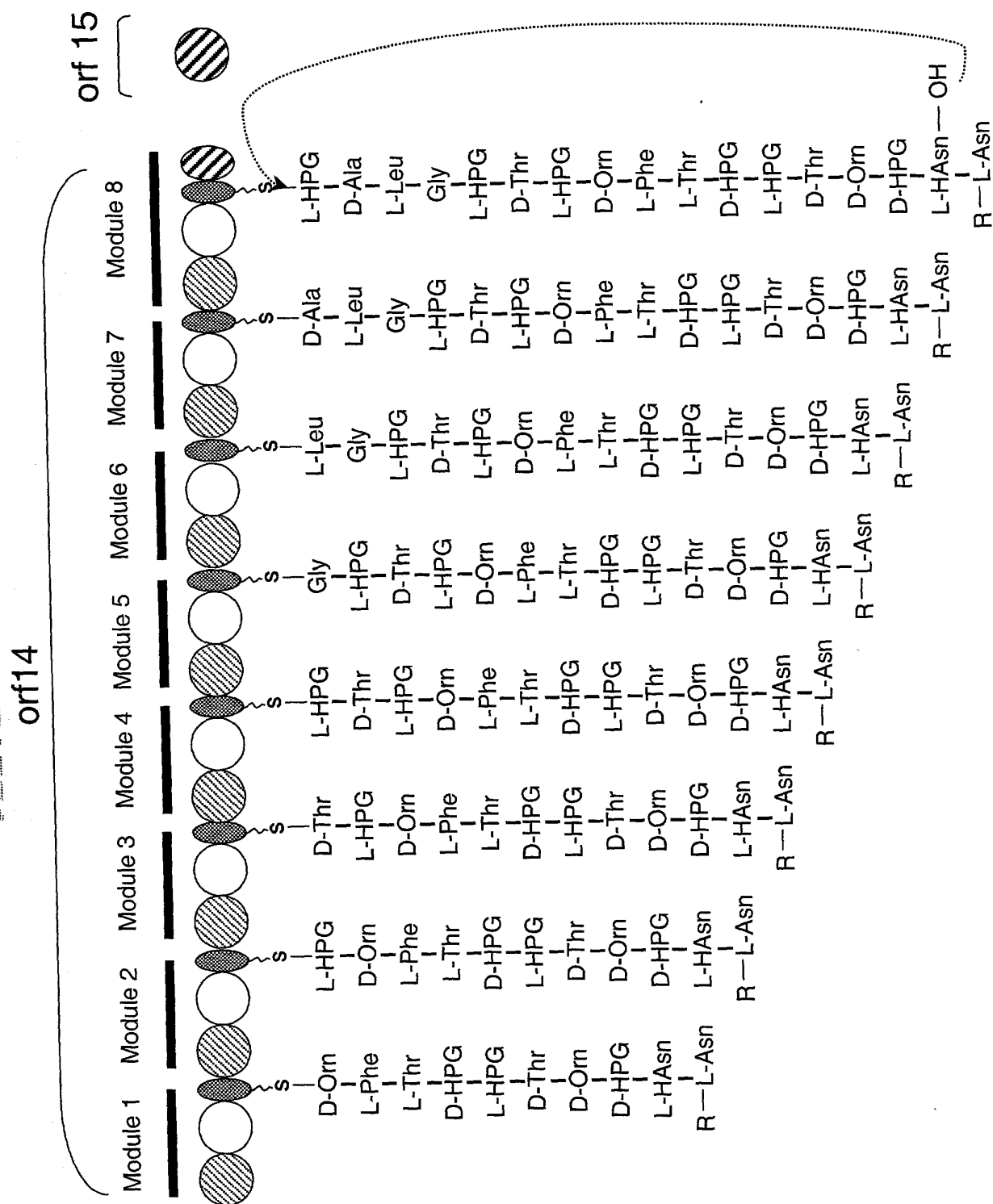


Figure 2B

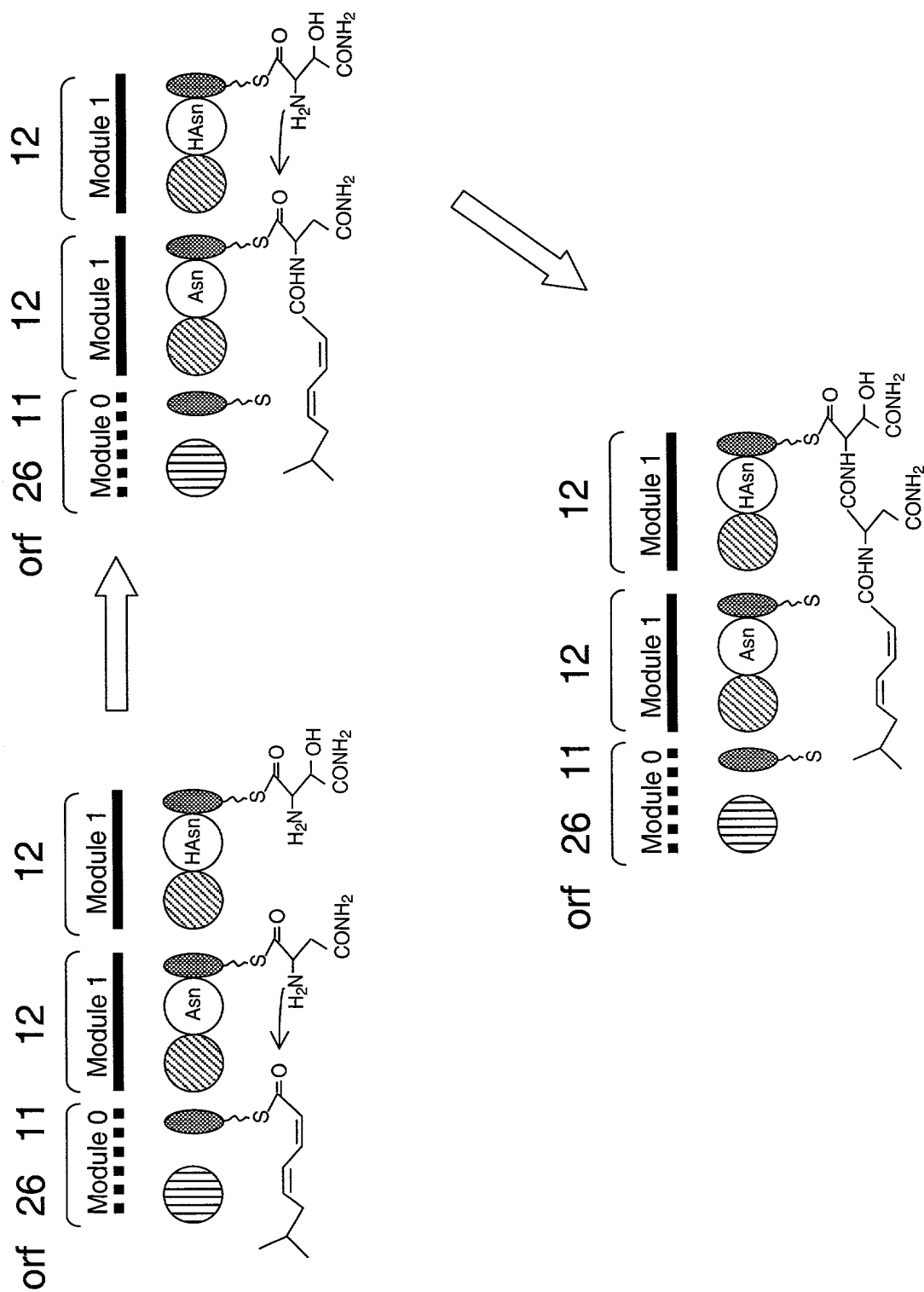


Figure 2C

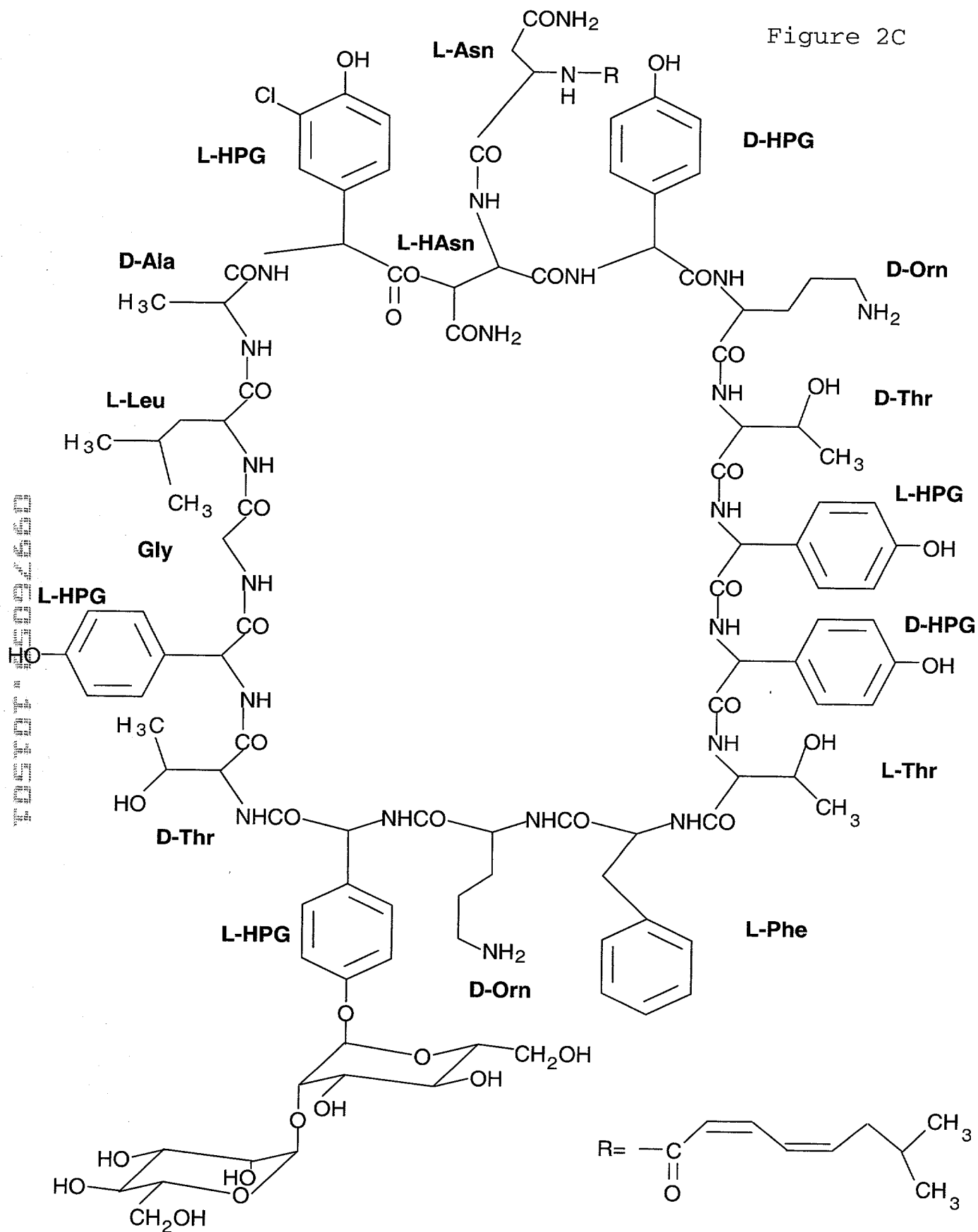


Figure 3A

```

Orf12 -----ERRRLLEDEWN-ATAAPSSDTVLARFEEQAARTPEAPAVVC
Orf13 |M1 -----ERSRLLVEWNDTARPVVSSVPALFAKRVAATPDATAVVG
Orf13 |M2 -----NATAVPAQPALVPELFTAQAARTPTWPAVLT
Orf13 |M3 -----DRLLTAWNEAREPAPP-VTLPDFDRQARRTPBAVALTA
Orf13 |M4 -----EIERVVHSWNDTARPVVSSVPALFAEQVAAAPDATAVVG
Orf13 |M5 -----ERSRLLVEWNDTARPVVSSVPALFAEQVAAAPDAVAVVG
Orf13 |M7 -----TVPELVAAQVARRPGAVALSRS
Orf14 |M1 -----NDTAAPAPAGLVPDFLFAAQAARTPDAAVAVAG
Orf14 |M2 -----NDTARRVRQASVPELFAERVAAAPGAPAVAA
Orf14 |M3 -----EESRLMLAAGEEPAPALPEITVAALVAEQCARTPGAVAVTG
Orf14 |M4 -----NETRRAVTRASVPELFAKQVAATPDAAVAVAG
Orf14 |M5 -----ERRLVLTGWNDTAAVPAVAVPELIERRAAAEPEAGAVVC
Orf14 |M6 -----ERREVLRTPNATARDVAAATLPAIVGEWARTTPGATAVTA
Orf14 |M7 -----EREAVLSGGNGGTAPVPVTTVPALFAEQARRTPGAVAAALS
Orf14 |M8 -----ERSRLLVEWNDTARPVVSSVPALFAERVAAAPDAVAVVG
Orf17 -----RTLTLGLFAEQVAAARPTAVAVSD
GrsA_Adomain MLNSSKSILIHQNKNGTHEEEQYLFVNNTKAEYPRDKTIHQLFEEQVSKRPNNVAIVC

```

```

A1 A2
Orf12 GDVVTYAELEAGANRLARVLRRAGAGPESVVALCLPRGPEVVTGILAAWKAGAAAYLPVD
Orf13 |M1 EGVSWSYRELDRRSDVLARLLVAAGVGVEPVVVALERSPEVLSAFLAVAKAGGVFVFPVD
Orf13 |M2 AGAEMSYAELEERSNRLARWLARGVGADDRVALMMRRGPELMVAAILAVLKAGAAAYLPVD
Orf13 |M3 DGVSLTYRELSERANRIARLLTSRGIGFESLVGVVLPASADLVVALLGVQAGAAAYVFPVD
Orf13 |M4 EGVSWSYRELDARSDALARSIVAAGVGVEPVVVALERSPEVLSAFLAVAKAGGVFVFPVD
Orf13 |M5 EGVSWTYRELDARSDALARSIVAAGVGVEPVVVALERSPEVLSAFLAVAKAGGVFVFPVD
Orf13 |M7 EDGEITYAELEARAGRLAAVLRRRGIGFESRVAVLLPRGVEQVVAFLAVVRAGGTYPVD
Orf14 |M1 PDRELTYAELEDERSGRLARWLIRRGVAADTRVALVLSAELPVAILAVLKAGGAYLPVD
Orf14 |M2 GDLRWTYADLDARSDALARSIVAAGVTAESPVVVALERSADVLTAFLAVAKAGGVFVFPVD
Orf14 |M3 PDASLTAELEDERAARIARWLRRHGAGPGAACVLMERSAELVAVLLGVMRAGAAAYVFPVD
Orf14 |M4 EGVSWSYRELDVRSDALARSIVAAGVGIESPVVVALDRSPVPTAFLAVAKAGGVFVFPVD
Orf14 |M5 GDTMLRYGELEANANRLARLLVERGAGFESIVAVCLERSADLVVTLAVLKAGAAAYLPVD
Orf14 |M6 ENDRLTAELEDERANRLARSLIARGVGPGAVVGMMLPRSPGLVVAAMLATVKAAGAYLPVD
Orf14 |M7 EGMSLTYADLAARVNRLARHLVSLGAGFETVVGIAISRGLDMLVAVLAVGQAGAAAYLPVD
Orf14 |M8 EGVSWSYRELDRRSDVLARSIVAAGVGLESPVVVALERSADVLTAFLAVAKAGGVFVFPVD
Orf17 DRGRHTYRELDWESGRLARGRLKAGVRDGDVGVCLDRSAELVAVLLAVLKAGAAAYVPVD
GrsA_Adomain ENEQLTYHELENVKANQLARIFIEKGIGKDTLVGIMMEKSIDLFIGILAVLKAGGAYVFPVD

```

```

Orf12 TELPAERVAYLLGDSAAAVRLG--TAETLAALPDGP-----AADVDVHA
Orf13 |M1 LSWPQARVDVAVDCAARVAVA--DRPMSGLTVVSAGL-----GGDSAVVSA
Orf13 |M2 PDLPRDRVDYLLADAAPAFVLA--ERATAPWVPVA-----GGIPVLVVDA
Orf13 |M3 ADYPAERIGYILGDAGAVCVLT--VDTAGAVPPG-----VPKLVLDH
Orf13 |M4 LSWPQARVDVAVDCAARVAVA--DRPMSGLTVVPA-----GGDSAVVSG
Orf13 |M5 LSWPQARVDVAVDCAARVAVA--DRPMSGLTVVSAGL-----GGDSAVVSG
Orf13 |M7 PAYPRDRVDYLLDAEPACLLT--VAGHRAAFAAP-----AVVELDD
Orf14 |M1 PAQPPRIADIVADAAPALVLA--QASTADVADASPALVLPASDGVPTGAVPVHLLDS
Orf14 |M2 LSWPRARVDVAVDCAAWIAVA--DRPMTGLTVVPAN-----VPCLAIDD
Orf14 |M3 PAYPAERIRFVVTDAACVVS--ESASAGLVPDG-----VPCLAIDD
Orf14 |M4 LSWPQARVDVAVDCAARVAVA--DRPMTGLTVVPA-----AQRIVLGD
Orf14 |M5 PGYPAGRIAYMLADARPALLVTSPAVASGDSLDPGG-----AQRIVLGD
Orf14 |M6 PGYPAPRLARMVEDAAPALLLA--TAGTADAVPAGP-----QRLLLDD
Orf14 |M7 PSYPDERKEFMLTDAGAAVYLT--LASDADRVPVPGTP-----AAAVVLDE
Orf14 |M8 LSWPQTRIDAVIAD-S-----RPVLVLDSDVLDL-----AAAVVLDE
Orf17 AAYPADRIAYTVGDAGLAVVVT--TSADFDPV-DG-----VRLAPES
GrsA_Adomain IEYPKERIQYILDDSQARMLLT--QKHLVHLIHNQFN-----GQVEIFEE

```

Figure 3A

Figure 3A cont'd

A3

Orf12		PEIARE-----SP-----SPLRLEPLPDQLAYVIYTSGSTGLSKGVGVSHGGLANYVGWAS
Orf13	M1	DLTADRAVVLPSRPV-----GAAVYRMYTSGSTGRPKGVVTHQNLDLAT---
Orf13	M2	PAVAAEVAHSGEAVTDRDRRAALRGGHAYVIYTSGSTGRPKGVLI THDGLANLTL-DH
Orf13	M3	PETVTALAACDTAPLGEAERAGELLPEHPAYVIYTSGSTGTPKGVLI PHRNVLFAATR
Orf13	M4	DQVGDSAVVLPAGPVP-----GAAVYRMYTSGSTGRPKGVVTHQNLDLAT---
Orf13	M5	DLTADRAVVLPSRPV-----GAAVYRMYTSGSTGRPKGVVTHQNLDLAT---
Orf13	M7	PATAAEIADAEPEPP-----VAVRPTHSAyliYTSGSTGRPKGVVTHRGVAALVATQA
Orf14	M1	PAVRDEVAQCAGAVTDADRRGVLLGGHAAVYIYTSGSTGRPKGVVSHDAFANLVL-DQ
Orf14	M2	-RAGDPAVALPPRPLP-----GAAVYRMYTSGSTGRPKGVVTHQNVDLVT---
Orf14	M3	P-----AAAAEPAEPGDDPGDAAGPRPDPAYIIYTSGSTGTPKGVVSHRNVALLTATR
Orf14	M4	DAAGDPAALPPRPLP-----GAEVYRMYTSGSTGRPKGVVTHQNLDLAT---
Orf14	M5	PDTAALDGLAGTDLVLSERRGVTHPAHPAYVIYTSGSTGRPKGVVPHGALTNFVAAMS
Orf14	M6	PGTAAELARLDGDPIDREETHPLRPGHPAYLMFTSGSTGRPKGVLPVPHAGIDRMVR-RS
Orf14	M7	PVTAARIAGLDPADLTDADRVAPLLPAHRAVYIYTSGSTGRPKGVAVEHRTVNLWSAA
Orf14	M8	-----AAEADLPRVPA-----GAGVYRMYTSGSTGRPKGVVTHQNLDLAT---
Orf17		-----LAEAGDDPGIPLATPAG--PERPAYVIYTSGSTGRPKGVVPHANVSALLDATR
GrsA_Adomain		DTIKIREGTLNHLVPSK-----STDLAYVIYTSGTTGNPKGTMLEHKGISNLKVFPE

* : : * * : * * . * *

A4

Orf12		VLYGGLSAP---LHSSLAFDLTVTSVFPVPLVCGGSVVVSAAGGGRGLASLLAAGDG--FS
Orf13	M1	-DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNGGTVVVAPQRSID-ATVLKDLIRAHDLT
Orf13	M2	GRFGLGPGARVAQFASPGFDMFVDEWSMALLAGAALTFFVPPERRL-GADLAAFLAEYGV
Orf13	M3	GSPHFGEGDVWSWFHSAFDFEIVWELWGALLHGGRVVMVFPFAVSRSPRDFWELLVREVT
Orf13	M4	-DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNGGTVVVAPQRSID-ATVLRDLIRGHELT
Orf13	M5	-DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNGGTVVVAPRRSID-ATVLRDLIGAHELT
Orf13	M7	ERLAVTGESRVLQFASVGFDAISIWEMVMALCAGATLVVAPADDLLPGPALAATLSGHA
Orf14	M1	RRLGIGPGSRVAQFASPGFDMFVDEWSMALLAGALVIVPPERRL-GADLAAFLTERGVT
Orf14	M2	-DRCWGPTPRVLFHAPHAFDASSFELWVPLLTGGTVVVPAGESID-TGVLRLIRAH
Orf14	M3	PLFGFAGDEVWSWFHSAFDFEIVWELWGALTGGGRVVPVYAVSRSPRDFWELLVREVT
Orf14	M4	-DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNGGTVVVAPGRSID-AAVLGELIRAH
Orf14	M5	DRLALGAGDRLLAVTTVAFDHIVLELYVPLVGGAGVVVAEDAVVRDPAVAALLDRH
Orf14	M6	TCLQLAPDDVLPPLSSVSFDAATFEIWGALLNGATLAVAPAETLS-VAELRAFLADR
Orf14	M7	GRFGGADFARTLAATSLNFDFEIVWELWGCLLTGGHLVVPYVWVSRSPQFHDLLA
Orf14	M8	-DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNGGTVVVAPRRSID-ATVLRDLVRG
Orf17		EEYALGPGDVWVTFHSAFDFEIVWELWGCLLTGGHLVVPYVWVSRSPQFHDLLA
GrsA_Adomain		NSLNVTEKDRIGQFASISFEDASVWEMFMALLTGASLYIILKDTINDFVKFEQYINQ

* * . * * : .

A5

Orf12		LVKVVPGHLRLLAELVPAGEMAAGV----SLVAGGEVLGGDVREWLSRVPGS--VVVNE
Orf13	M1	HVHVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVKDANPGL--RVRL
Orf13	M2	HATLPP---AVVGITPDGVLPPSF----VLGVGGDVLPGLDARR--WLRDGR--VIFNS
Orf13	M3	VLSQTP---SAFYQLAAAA-DDTPD-ALRVVVEGGEALDPGRLAGWRERRPDG-PRIVNM
Orf13	M4	HVHVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVREANPGL--RVRL
Orf13	M5	HVHVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVKDANPGL--RVRL
Orf13	M7	HATLPP---AVLAASAPGDLAPLA----VLVSAGEALGPDLVR---QFAPGR--AIVNA
Orf14	M1	HATLPP---AVVATLPEESLPSF----VLDTGGDALPDDLARR--WLRDGR--WLGNS
Orf14	M2	HVHVTA---GLLRVLA--DPSCFAG--LTEVLTGGDVVPAAEAVRRVLDANPGV--RVRL
Orf14	M3	VLSQTP---SAFAQLMAAAGDDDRD-ALRFVVEGGEALDPGRLAGWLARRPDK-PRIVNM
Orf14	M4	HVHVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVMEANPGL--RVRL
Orf14	M5	IVQATP---ALWQALLAGHADAVRD---VRLVVGGEALPPALAG--RMAAAGR--GVTNL
Orf14	M6	KLFLTT---GLLHEVIDADVTALAG--LKAVYTGDDVLSPAHCRSLLDVVPGL--EITYNA
Orf14	M7	LVSGVP---SAFSRVLDRGDIAART---RSVVLAGEALTADVNNATRAALPGV--RVAN
Orf14	M8	HVHVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVKEANPGL--RVRL
Orf17		VLNQTP---SSTQLVAADRGAERDLAVRLVIEGGEPLDARTVLPWLDRRPEARCRIVNM
GrsA_Adomain		VITLPP---TYVVHLDPERILSIQT-----LITAGSATSPSLVNKKVKVT-----YINA

: * :

Figure 3A cont'd (2)

A5

Orf12 YGPTETTVGCSVFSVAAGDVVGD--VVPVGRPVANTRFLVLDGLRPVPAGVAGELYVAG

Orf13 M1 YGPTETVTLCAQHLLD-DG-----VPIGRPLDNTRVYVLDLQLPVPVGVGTGELYVAG

Orf13 M2 YGPTETTVNAATWR-AEAGDWGS--VAPIGTPVPNLRAYVLDGWLRPVPVGVAGELYVSG

Orf13 M3 YGITHETTVHVTHQDLAPAD-TTG--S-PIGRGIPGLSVYVLDALRPVPPGVAGEVYVAG

Orf13 M4 YGPTETVTLCAQHLLV-DG-----VPIGRPLDNTRVYVLDLQLPVPVGVGTGELYVAG

Orf13 M5 YGPTETVTLCAQHLLD-DG-----VPIGRPLDNTRVYVLDLQLPVPVGTGVVGEVYVAG

Orf13 M7 YGPTETTVCATASAPLGPEDPPH-----IGAPVADSRVYVLDLALTPVPPGVGTGELYVSG

Orf14 M1 YGPTETTVNAATWR-CEPGTWEG--ATPIGRPVANLRAYVLDGRLRPVPVGVGTGELYVSG

Orf14 M2 YGPTETVTLCAQHVVREPSPV-----LPIGRPLDNTRVYVLDGLLQPVPVGVGTGELYIAG

Orf14 M3 YGITHETTVHTTYQHIAFG--TTG--S-VIGRGLPGFGLYVLDALRPVPAGVAGEVYVAG

Orf14 M4 YGPTETVTLCAQVLDGTG-----VPIGRPLDNTRVYVLDLQLPVPVGVGTGELYVAG

Orf14 M5 YGPTETTVWATVADLGA-SPAG---FVPIGTPLRNTRAFVLDLALRPVPVGVGTGELYLAG

Orf14 M6 YGPTETTTITTLHR-VRPEDLDAGTGVPIGVPISTDRVYVLDLALRPVPVGVAGELYTSG

Orf14 M7 YGITHETTVYSTAWHTDR-DVTGG--AAPIGRPVTNTRAYVLDLRLTPVPPGVGTGELYLAG

Orf14 M8 YGPTETVTLCAQHLLD-DG-----VPIGRPLDNTRVYVLDLQLPVPVGTGVVGEVYVAG

Orf17 FGITETTVHVTAVDVTRAALAG--SRSVGRPLPGWAVRVLDQRREVPPGVGEIYVVG

GrsA_Adomain YGPTETTTCATTWATKETIGHS---VPIGAPIQNTQIYIVDENLQLKSVGHAGELCIG

: * * * . : : * : . : * : . * * * :

A6

Orf12 SQVARGYVGRSGLTASRFVACPFPG-VGERMYRTGDLVRVLAG-GDLVGVGRVDEQVKIRGY

Orf13 M1 AGVARGYAGMPGLTAERFVADPFNT-GGRLYRTGDLVRWTDGVLHFAGRADDQVKIRGY

Orf13 M2 AGLARGYLNRAGLTAERFVACPFEP-GERMYRTGDLVRWTAEGRLVFAGRSDDQVKIRGF

Orf13 M3 RQLARAYLGRAALTGTRFVACPFPLPAGERMYRTGDRARWSR-GRLLQFAGRTDDQVQIRGF

Orf13 M4 AGLARGYAGMPGLTAERFVADPFSS-VGRLYRTGDLVRWTDGVLHFAGRADDQVKIRGY

Orf13 M5 SGLARGYAGMPGLTAERFVADPFNT-GGRLYRTGDLVRWADDGVLHFAGRADDQVKIRGY

Orf13 M7 ASLARGYAGRAALTAEFVACPFAP-GERMYRTGDRARWDAAGRLTFAGRADDQVKIRGF

Orf14 M1 AGLARGYLNRAGLTAGSFVACPFEP-GERMYRTGDLVRWDARGRLVYAGRADDQAKIRGF

Orf14 M2 AGVARGYADMPGTTAEFVADPFSS-VGRLYRTGDLVRWTDGVLHFAGRADDQVKIRGY

Orf14 M3 PQVARGYIGRPGLTAERFVADPFAP-GERMYRTGDLVRWTDGRLVFAGRSDDQVKIRGF

Orf14 M4 AGLARGYAGMPGLTAERFVADPFSS-VGRLYRTGDLVRWTDGVLHFAGRADDQVKIRGY

Orf14 M5 DQLARGYHGRAGLTAEFVADPFPG-RGERMYRTGDRVRWTRGGSLEFLGRVDDQVKIRGF

Orf14 M6 IGLAHGYAGRPAPTAEFVACPFAP-GERMYRTGDLVRWTDGRLVFAGRADDQVKIRGF

Orf14 M7 AQLARGYLGRPGLTAEFVACPFPGGERMYRTGDRVRWNADGDLVFAGRADDQVKIRGF

Orf14 M8 SGLARGYAGMPGLTAERFVADPFSS-VGRLYRTGDLVRWTDGVLHFAGRADDQVKIRGY

Orf17 AGVAIGYLNRPGLTAERFVADPFSS-VGRLYRTGDLVRWTDGRLVFAGRADDQVKIRGF

GrsA_Adomain EGLARGYVGRSGLTASRFVADPFPG-VGERMYRTGDLVRVLAG-GDLVGVGRVDEQVKIRGY

: * * . * . * * * : * : * * * : * : . * * * : * * :

A8

Orf12 RVEPDEVLLVVAGHPRVAGAAVVARPDVAGE---RQLVAYVVVAGEPAG---LAESVRAH

Orf13 M1 RVEPGEVAVLAQHDPDVSQVAVVVREDTPGD---KRLVAYVVVGG-----DIEAY

Orf13 M2 RIEPGEVAVLAAGPGVSAQAVIVREDVPGD---KRLVAYVVVGG---D---VEALRSY

Orf13 M3 RIEPGEVQAVVAHPEIAAAVAVVVREDVPGD---PRLTAYVVVAGPRTAPAAVAETVRRF

Orf13 M4 RVEPGEVAVLAQHDPDVSQVAVVVREDTPGD---KRLVAYVVVGG-----DVEAY

Orf13 M5 RVEPGEVAVLAQHDPDVSQVAVVVREDTPGD---KRLVAYVVVGG-----DVEAY

Orf13 M7 RVEPGEVAVLGEHPAVARAAVVARTDGPQG---ARLVAYLVVADP---AGPDLAADVRAV

Orf14 M1 RVEPGEVAVLAAGPGVNVQAVIVREDVPGD---KRLVAYVVVGG---D---VETLRSY

Orf14 M2 RVEPGEVAVLAALPGVSAQAVIVREDVPGD---KRLVAYLVVAAPE-----TVEAARAH

Orf14 M3 RIEPGEVAVLAAGPGVSAQAVIVREDVPGD---KRLVAYVVVGG-----DAETLRSH

Orf14 M4 RVEPGEVAVLAQHDPDVSQVAVVVREDTPGD---KRLVAYVVVGG-----DVEAY

Orf14 M5 RIELGEVAAALAAFGPVARAAAVREDVPGD---RRLVGYVVVPAAGEPE--PDPAAVRAH

Orf14 M6 RVEPGEVAVLAALPGVSAQAVIVREDVPGD---KRLVAYVVVPAAPDEDGDALAEVRAV

Orf14 M7 RIEPGEVQAVVARQAGVARAVVLRSDSPGD---ARLVAYVVVPADRADRRALAAATVRS

Orf14 M8 RVEPGEVAVLAQHDPDVSQVAVVVREDAPGD---KRLVAYVVVGG-----DVEAY

Orf17 RIELDEIRGVLTACAGVAAAVVIRSTPDDPATARLDAYVVVAEAG-----ATPPVAEH

GrsA_Adomain RVELEEVSILLKHYISETAVSVHKDHQEQ---PYLCAYFVSEKHIP-----LEQLRQF

* : * * : : : : : * : * * :

Figure 3A cont'd (3)

A10

Orf12	VAERLPEYMPAAVVTLDLDEIPLT	VNGKVDRAALPEP-----
Orf13 M1	GQERLPGYMPVPSAFVHLDALPLT	SNQKVDRAALPAPSMESG-----
Orf13 M2	AQQR LPGYMPVPSAFVHLDALPLT	VNGKLDRAALPVPDLARG-----
Orf13 M3	AADRLPAYMLPSAVVVLDALPLT	DHGKLDRAALPAPQHT-----
Orf13 M4	AQERLPGYLVPSAFVHLDALPLT	SNQKVDRAALPAPSVESGV-----
Orf13 M5	AQERLPGYMPVPSAFVQLDALPLT	SNQKVDRAALPAPSMESG-----
Orf13 M7	AAATLPAHLLPAAFVPLDRLPLT	TNGKLDRAALPEPETGAG-----
Orf14 M1	AQQR LPGYLVPSAIVALAELPLT	PSAKVDRAALPVPD-----
Orf14 M2	AEQR LPSYLVPSAFVQLDALPLT	GNQKVDRAALPAP-----
Orf14 M3	AQQR LPGYLVPSAFVHLDALPLT	VNGKLDRAALPVPD-----
Orf14 M4	AQERLPGYLVPSAFVHLDALPLT	SNQKVDRAALPAPSVESG-----
Orf14 M5	VAAQLPAYMPVSAVVVLPDLPLT	ANGKLDRAALPAPDYGAASAGRAPADE--
Orf14 M6	AARQVPDYLMPAATVVLPDLPLT	SSGKVDRAALPAPDVPGG-----
Orf14 M7	TARELPAYLVPAVVVLDLPLT	ANGKLDRAALPAPGL-----
Orf14 M8	AQERLPGYMPVPSAFVHLEALPLT	ANQKVDRAALPAPE-----
Orf17	AARMLPAYMCPATFTFLDALPMT	PNGKVDRAALPEP-----
GrsA_Adomain	SSEELPTYMIPSYFIQLDKMPLT	ENGKIDRAALPEPDLTFGMRVDYEAPRNE

* : * : * : * : * : *

09976669 04504

Figure 3B

				235	236	239	278	299	301	322	330	
	Orf13	M1	HPG	D	A	Y	H	L	G	L	L	HPG
	Orf13	M4	HPG	D	A	Y	H	L	G	L	L	
	Orf13	M5	HPG	D	A	Y	H	L	G	L	L	
	Orf14	M2	HPG	D	A	F	H	L	G	L	L	
	Orf14	M4	HPG	D	A	Y	H	L	G	L	L	
	Orf14	M8	HPG	D	A	Y	H	L	G	L	L	
emb	CAB38518.1	Cda1	M6	HPG	D	V	Y	H	L	G	L	
emb	CAA11795.1	CepB	M2	HPG	D	A	V	H	L	G	L	
emb	CAA11795.1	CepB	M1	HPG	D	I	F	H	L	G	L	
	Orf13	M3	Thr	D	F	W	S	V	G	M	V	Thr
	Orf14	M3	Thr	D	F	W	S	V	G	M	V	
	Orf17	M1	Thr	D	F	W	N	I	G	M	V	
gb	AAC38442.1	AcmB	M1	Thr	D	F	W	N	V	G	M	
emb	CAB38518.1	Cda1	M2	Thr	D	F	W	N	V	G	M	
emb	CAA09819.1	FenD	M2	Thr	D	F	W	N	I	G	M	V
	Orf13	M2	Orn	D	M	D	T	D	G	S	V	Orn
	Orf14	M1	Orn	D	M	D	T	D	G	S	V	
gb	AAC06347.1	BacB	M1	Lys	D	A	E	S	I	G	S	
gb	AAC82550.1	FxbC	M1	5hOrn	D	M	E	N	L	G	L	
gb	AAC82550.1	FxbC	M3	5hOrn	D	M	E	N	L	G	L	I
	Orf12	M1	Asn	D	L	T	K	V	G	E	V	Asn
emb	CAB38517.1	Cda2	M3	Asn	D	L	T	K	V	G	E	
gb	AAC06348.1	BacC	M5	Asn	D	L	T	K	I	G	E	
gb	AAC45930.1	TycC	M1	Asn	D	L	T	K	I	G	E	
	Orf13	M7	Phe	D	A	W	T	V	A	A	V	Phe
emb	CAA33603.1	GrsA	M1	Phe	D	A	W	T	I	A	A	
gb	AAC45929.1	TycB	M3	Phe	D	A	W	T	I	A	G	
gb	AAC06348.1	BacC	M2	Phe	D	A	F	T	V	A	A	
	Orf14	M5	Gly	D	I	L	Q	L	G	L	V	Gly
emb	CAB38517.1	Cda2	M2	Gly	D	I	L	Q	L	G	L	
emb	CAB15186.1	DhbF	M1	Gly	D	I	L	Q	L	G	L	
gb	AAF17280.1	NosC	M2	Gly	D	I	L	Q	L	G	L	
	Orf14	M6	Leu	D	A	F	F	Y	G	A	T	Leu
emb	CAA82227.1	CssA	M2	Leu	D	A	W	L	Y	G	A	
emb	CAA82227.1	CssA	M3	Leu	D	A	W	L	Y	G	A	
gb	AAC06346.1	BacA	M3	Leu	D	A	W	F	L	G	N	
	Orf14	M7	(Ala)	D	V	F	S	V	A	I	V	(Ala)
gb	AAC06348.1	BacC	M2	Phe	D	A	F	T	V	A	A	
gb	AAC83656.1	PchE	M1	Cys	D	L	F	N	L	S	L	
emb	CAA82227.1	CssA	M1	Ala	D	V	F	I	Y	A	A	

65767459

[illegible]

AL4

DWLRMMDRYRVTSISAAPNFAYDLCVRAVRDEQIAGLDLSRIRTLYNGSEP
RWMHMLMASDFHAFSAAPNFAFELAARRTTDDDMAGRDLGNILITILSGSER
RWMQLLAKHRAQTSISAPNFGFELAVRRTSDDDMAGLDLGHVRTIVTGAER
RWLRVRSRYRAHFTSGGPNFAYDLCDVRVGEDERAGLDLSGWKVAYNGAEP
RWLKTLSERRGFTSGGPNFAYELCVRKISDEQKAGLDLSSWELAFCGAEP
LWMKKAHEHKASILSSPNFGGYNFLKFLKDNKSYDWDLSHIRVIANGAEP

:::***:::***

Figure 3C(2)

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

AL5
VNPATVRAFTERFAPFGLHTHAVNPCYGMAEFTAYVSTKVFEAPAVFLPA
VQAATIKRFADRFAFNLQERVIRPSYGLAEATVYVATSKPGQPPETVDF
VNVATLRRFTERFAPFNLSETAIRPSYGLAEATVYVATAGPGRAPKSVCF
VRADTLRRFTDRFAPHGFTPGAHFPTYGLAEATLLVATGPKGVPPRTLTA
IRPDTLEAFSKAFEPGCFRREAFYPCYGLAEGTLIVTGVSKGRAARVEHF
ILPELCDEFLTRCAAFNMKRSAILNVYGLAEASVGATFSNIGERFVPVYL
: * : : : : : *

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

DPRALEDAASPALRPADP-AAAREIP---GVGRV-PDFEVLIVDPDGLRP
DTELSAGH---AKPCAGGG-ATSLIS---YMLPRSPIVRIVDSDTCTE
DYQQLSVGQ---AKRAENGSEGANLVS---YGAPRASTVRIVDPETRME
DRAALRAGR---LRPAGPGEAGLELV---GNGTAGLDTTLRIVDPATARE
QREALEAHR---AVAASSPGEAARDTVRHVSCGTVPVDEQILVVDPETRTA
HRDHLNLGE---RAVEVSKEDQNCASFVEVGKPIDYCQIRICN-EANEG
* : : : : : *

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

AL6
LPEGRVGEIWLRGPGAGAGYWGRTLNPGIFDARPAAGD---QDGGWVVT
CPDGTVGEIIVHGDNVNGYWKPDDESERTFGGKIIVTPSPGTPEGPWLRT
NPAGTVGEIIVQGDNVGLGYWRNPQQTATFRARLVTPSPGTSEGPWLRT
CPPGEVGEVWVRGPGVARGYFGRPRESAPLLAARLPGG-----EGPYLRT
LPPGHIGEIVWRGPGSVAGGYWLRPEETARTFQARLAGG-----TEAPWLRT
LEDGFIGHIQIKGENVTQGYNNPESTNRALTP-----DGWVKT
* : : : : : *

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

AL6 AL7
GDLGALTGGELFLTGRLKELLIVHGRNLAPHDLEREARAAHDAVDHQIGA
GDSGFVTDGKMFIIGRIKDLLIVYGRNHSPDDIEETIQEITRGR----CA
GDLGVIFEGELFIIGRIKELLVVDGANHYPEDIEETIQEITGGR----VV
GDLGALHDGELFLTGRHKDLIVIRGQNHHPHDLERTAEQAHPALRPTCAA
GDLGFLHDGELFVSGRRKDLLVIRGRNYPQDLELTVERSHPALRPGCAA
GDLGFIRKGNLVVTGREKDIIFVNGKNVYPHDLERVAIELEDIDLGRVA
*** : * : : : : * * * * * *

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

AFGVFPAP--DERIVLVQEVHPRTPLDLDELPR-----VASAVSRRLTVSFGV
AISVPGDRRTEKLVAIIELKKRGDSQDAMARLGAIKREVTSALSSSHGL
AIAVPDDR-TEKLVTIIELMKRGRTDEEEKNRLRTVKREVASAISRSHRL
AFAVPGDG-AERLVLVCELTSYRAVDPAA-----VAEAVRAALAARHGV
VFSVSVGA-SEEVVVQEVDRRYPGGDWDPD-----VIAAIRRDISQHAL
ACGVYDQETRSREIVLFAVYKKSADRFAP-----LVKDIKKHLVQRGGW
* : : : : : *

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

AL8
PVRNVLLVRRGTVRRTTSGKIRRTAVRERFLAGGITALHAELEPALRPVQ
SVADLVLVAPGSIPIITTSKGVRRGACVEQYRQDQFARLDA-----
RVADVVMVAPGSIPIVTTSGKVRRSASVERYLHHEFSRLDAMA-----
APHTLVVLRRGSIPIKTTSGKVRRGHCRATAYLDGTLVPVHTAVRLP-----
RVHAVVLKSGSLLKTSSGKVORGATREAYLEGQLDTSADAAQEPVGE-
SIKEILPIR--KLPKTTSGKVKRYELAEQYESGKFALESTKIKEFLEG--
: : : : * : : : *

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

AGAGR

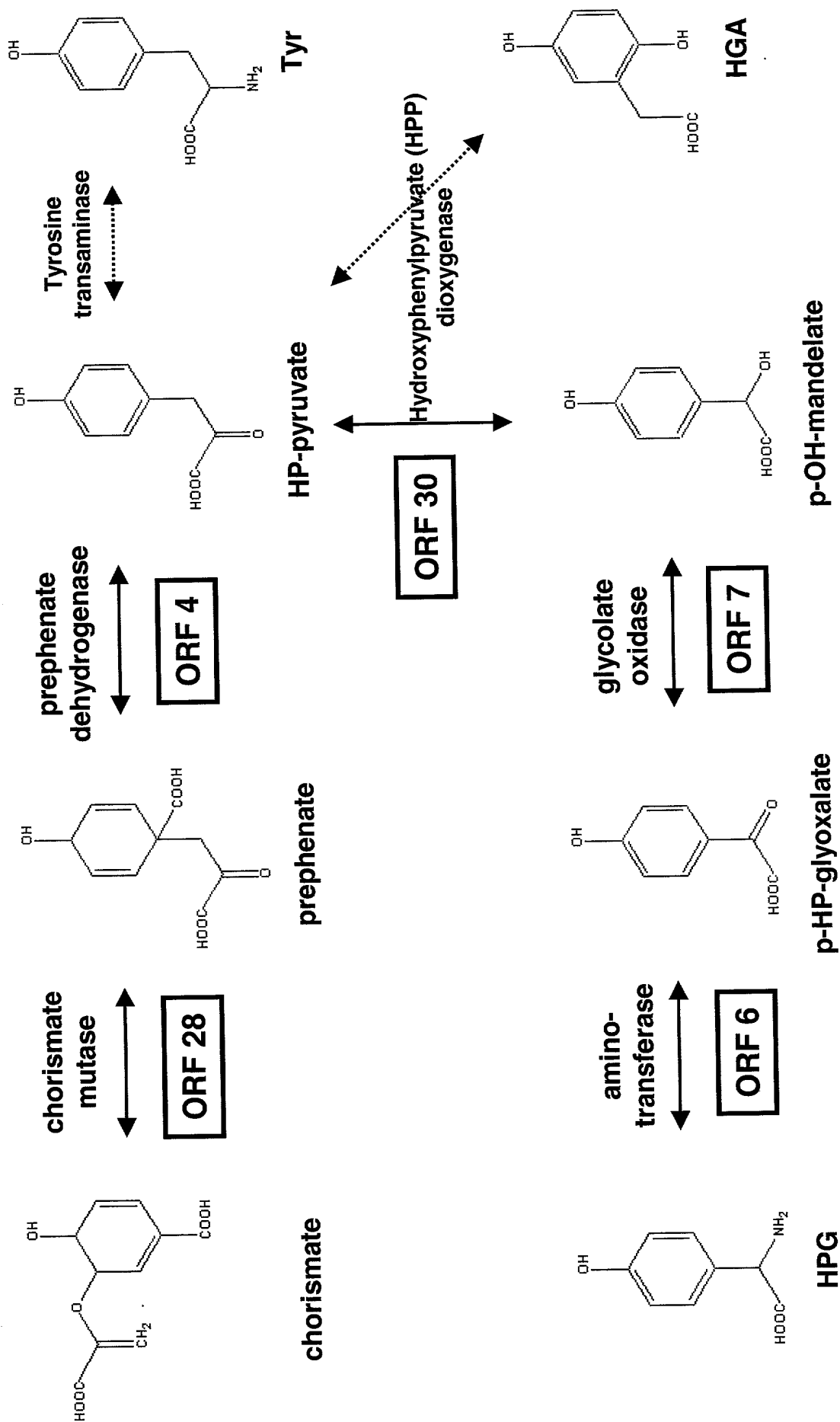


Figure 5A

pfam00753
1SML
ORF 10

LVEDDDGAALIDTGF^TAPAAKALLRL^LKDG--GKKIDAIILT^THAHAD^HHIGGVPELLER
LVQTPDGA^VLLDGGMPQ^MASHLLDNMKARGVT^RPRDLRLILLS^SHAHAD^HHAGPVAELKRR
VMQTEQA^AAVTDP-FISTDNRHGDRY^TLDL^L-PDHIDLVLITH^HGHQ^HDHIVLETLLQLR
::: .*. : * : . . . : : : * . * * . * *

Figure 5B

pfam00067
ORF 10

DPE--RFLDEN-GKFKKSYAFLPFGAGPRNCLGERLARMELFLFLATLLQRFELE
DPVLYRYIRDHVGQVD----MAFL-G-MECDGAPLNWLYKGLLT'KPVNKKMSAS
* * * : : : * : . : * * : * * * : * : . : : : . .

[illegible]

Figure 6

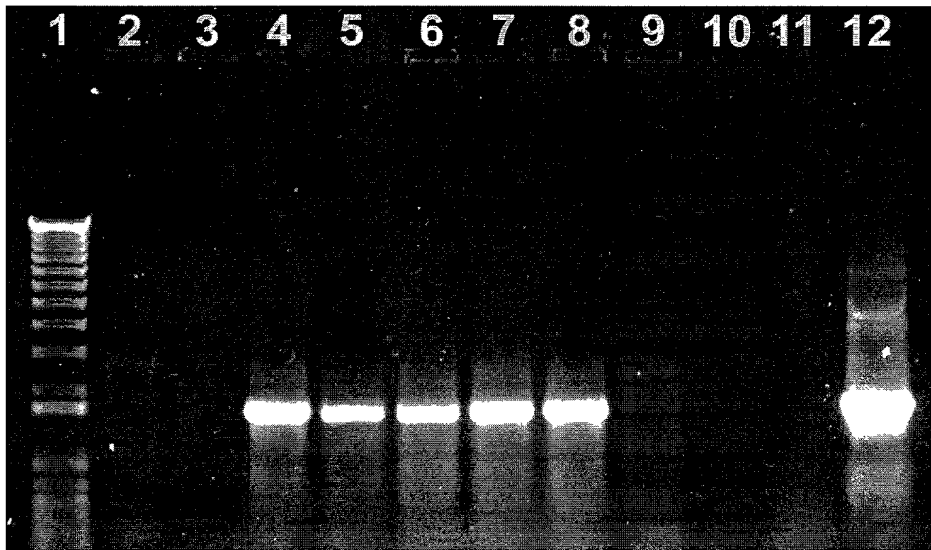


Figure 7

